

**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,106

Source: OIPE

Date Processed by STIC: 6-20-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001
TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT
Output Set: N:\CRF3\06202001\I873106.raw

```

4 <110> APPLICANT: Reinherz, Ellis L.
5      Freund, Christian
6      Li, Jing
7      Nishizawa, Kazuhisa
8      Wagner, Gerhard
10 <120> TITLE OF INVENTION: Cloning and Characterization of a CD2
11      Binding Protein (CD2BP2)
14 <130> FILE REFERENCE: 1062.1021-004
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/873,106
C--> 16 <141> CURRENT FILING DATE: 2001-06-01
16 <150> PRIOR APPLICATION NUMBER: US 60/111,007
17 <151> PRIOR FILING DATE: 1998-12-04
19 <150> PRIOR APPLICATION NUMBER: US 60/115,647
20 <151> PRIOR FILING DATE: 1999-01-13
22 <150> PRIOR APPLICATION NUMBER: PCT/US99/26993
23 <151> PRIOR FILING DATE: 1999-11-15
25 <160> NUMBER OF SEQ ID NOS: 25
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0

```

Does Not Comply
Corrected Diskette Needed

pp 2-8
The format
errors shown
were corrected.

ERRORED SEQUENCES

```

132 <210> SEQ ID NO: 2
133 <211> LENGTH: 341
134 <212> TYPE: PRT
135 <213> ORGANISM: Homo sapiens
137 <400> SEQUENCE: 2
138 Met Pro Lys Arg Lys Val Thr Phe Gln Gly Val Gly Asp Glu Glu Asp
139   1           5           10          15
140 Glu Asp Glu Ile Ile Val Pro Lys Lys Lys Leu Val Asp Pro Val Ala
141   20          25          30
142 Gly Ser Gly Gly Pro Gly Ser Arg Phe Lys Gly Lys His Ser Leu Asp
143   35          40          45
144 Ser Asp Glu Glu Asp Asp Asp Gly Gly Ser Ser Lys Tyr Asp
145   50          55          60
146 Ile Leu Ala Ser Glu Asp Val Glu Gly Gln Glu Ala Ala Thr Leu Pro
147   65          70          75          80
148 Ser Glu Gly Gly Arg Ile Thr Pro Phe Asn Leu Gln Glu Glu Met
149   85          90          95
150 Glu Glu Gly His Phe Asp Ala Asp Gly Asn Tyr Phe Leu Asn Arg Asp
151   100         105         110
152 Ala Gln Ile Arg Asp Ser Trp Leu Asp Asn Ile Asp Trp Val Lys Ile
153   115         120         125
154 Arg Glu Arg Pro Pro Gly Gln Arg Gln Ala Ser Asp Ser Glu Glu Glu
155   130         135         140
156 Asp Ser Leu Gly Gln Thr Ser Met Ser Ala Gln Ala Leu Leu Glu Gly
157   145         150         155         160

```

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158 Leu Leu Glu Leu Leu Pro Arg Glu Thr Val Ala Gly Ala Leu Arg
159 165 170 175
160 Arg Leu Gly Ala Arg Gly Gly Lys Gly Arg Lys Gly Pro Gly Gln
161 180 185 190
162 Pro Ser Ser Pro Gln Arg Leu Asp Arg Leu Ser Gly Leu Ala Asp Gln
163 195 200 205
164 Met Val Ala Arg Gly Asn Leu Gly Val Tyr Gln Glu Thr Arg Glu Arg
165 210 215 220
166 Leu Ala Met Arg Leu Lys Gly Leu Gly Cys Gln Thr Leu Gly Pro His
167 225 230 235 240
168 Asn Pro Thr Pro Pro Ser Leu Asp Met Phe Ala Glu Glu Leu Ala
169 245 250 255
170 Glu Glu Glu Leu Glu Thr Pro Thr Pro Thr Gln Arg Gly Glu Ala Glu
171 260 265 270
172 Ser Arg Gly Asp Gly Leu Val Asp Val Met Trp Glu Tyr Lys Trp Glu
173 275 280 285
174 Asn Thr Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met
175 290 295 300
176 Gln Thr Trp Val Ser Glu Gly Tyr Phe Pro Asp Gly Val Tyr Cys Arg

E--> 177

305 310 315 320 Lys Leu Asp Pro Pro Gly Gly Gln
179 <210> SEQ ID NO: 3
180 <211> LENGTH: 26
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 3

E--> 185

Gly Asp Ala Glu Leu Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr 1
187 <210> SEQ ID NO: 4
188 <211> LENGTH: 27
189 <212> TYPE: PRT
190 <213> ORGANISM: Caenorhabditis elegans
192 <400> SEQUENCE: 4

E--> 193

Gly Pro Asp Ser Glu Lys Tyr Gly Pro Tyr Met Ser Lys Asp Met Leu 1
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 27
197 <212> TYPE: PRT
198 <213> ORGANISM: Caenorhabditis elegans
200 <400> SEQUENCE: 5

E--> 201

Asp Pro Thr Glu Thr Arg Arg Gly Pro Phe Pro Lys Asp Gln Met Asn 1
203 <210> SEQ ID NO: 6
204 <211> LENGTH: 27
205 <212> TYPE: PRT
206 <213> ORGANISM: Caenorhabditis elegans
208 <400> SEQUENCE: 6

E--> 209

Asp Asp Arg Gly Thr Val Gln Gly Pro Tyr Gly Ala Ser Thr Val Leu 1
211 <210> SEQ ID NO: 7
212 <211> LENGTH: 29
213 <212> TYPE: PRT
214 <213> ORGANISM: Saccharomyces cerevisiae

5
format
error
causing
misaligned
amino
acids and
amino acid
numbers.

216 <400> SEQUENCE: 7

6/20/01

file:///C:/CRF3/Outhold/VsrI873106.htm

Input Set : A:\1062.1021-004.TXT
Output Set: N:\CRF3\06202001\I873106.raw

E--> 217

Asp Thr Gln Gly Gln Ile His Gly Pro Phe Thr Thr Gln Met Met Ser 1

219 <210> SEQ ID NO: 8
220 <211> LENGTH: 27
221 <212> TYPE: PRT
222 <213> ORGANISM: Saccharomyces cerevisiae
224 <400> SEQUENCE: 8

5

Same

E--> 225

Asp Ser Asn Gly Asn Ile Gln Gly Pro Phe Gly Thr Asn Asn Met Ser 1

5

227 <210> SEQ ID NO: 9
228 <211> LENGTH: 17
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Motif in CD2 binding region of CD2BP2
236 <221> NAME/KEY: VARIANT
237 <222> LOCATION: (1)...(2)
238 <223> OTHER INFORMATION: Xaa = Any Amino Acid
240 <221> NAME/KEY: VARIANT
241 <222> LOCATION: (3)...(3)
242 <223> OTHER INFORMATION: Xaa can be Tyr or Phe
244 <221> NAME/KEY: VARIANT
245 <222> LOCATION: (4)...(7)
246 <223> OTHER INFORMATION: Xaa = Any Amino Acid
248 <221> NAME/KEY: VARIANT
249 <222> LOCATION: (8)...(8)
250 <223> OTHER INFORMATION: Xaa can be Met or Val
252 <221> NAME/KEY: VARIANT
253 <222> LOCATION: (9)...(15)
254 <223> OTHER INFORMATION: Xaa = Any Amino Acid
256 <400> SEQUENCE: 9

E--> 257

Gly Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Thr 1

5

Same

259 <210> SEQ ID NO: 10
260 <211> LENGTH: 6
261 <212> TYPE: PRT
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: CD2BP2 binding region
268 <400> SEQUENCE: 10

E--> 269 Pro Pro Pro Gly His Arg 1

5

271 <210> SEQ ID NO: 11
272 <211> LENGTH: 70
273 <212> TYPE: PRT
274 <213> ORGANISM: Homo sapiens
276 <400> SEQUENCE: 11
277 Pro Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro
278 1 5 10 15
279 Pro Pro Pro Gly His Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro
280 20 25 30
281 Ala Pro Ser Gly Thr Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro

Same

E--> 282

35

40

45

Arg Pro Arg Val Gln Pro Lys Pro

RAW SEQUENCE LISTING
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Input Set : A:\1062.1021-004.TXT
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306 <210> SEQ ID NO: 14
307 <211> LENGTH: 8
308 <212> TYPE: PRT
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Flag Epitope
314 <400> SEQUENCE: 14

E--> 315 Asp Tyr Lys Asp Asp Asp Asp Lys 1

5

317 <210> SEQ ID NO: 15
318 <211> LENGTH: 31
319 <212> TYPE: PRT
320 <213> ORGANISM: Gallus gallus
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Flag Epitope
325 <400> SEQUENCE: 15

Same

E--> 326

Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Ser Asn 1

5

328 <210> SEQ ID NO: 16
329 <211> LENGTH: 38
330 <212> TYPE: PRT
331 <213> ORGANISM: Drosophila melanogaster
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Flag Epitope
336 <400> SEQUENCE: 16
337 Glu Val Thr Trp Glu Phe Lys Trp Ser Gln Asp Glu Thr Asp Ile Gln

E--> 338

1 5 10 15 Gly Pro Phe Ser Thr Glu Lys Met

340 <210> SEQ ID NO: 17
341 <211> LENGTH: 34
342 <212> TYPE: PRT
343 <213> ORGANISM: Leishmania major
345 <220> FEATURE:
346 <223> OTHER INFORMATION: Flag Epitope
348 <400> SEQUENCE: 17
349 Val Trp Met Met Arg Trp Lys Ala Lys Pro Thr Val Gln His Gly Pro

Same

E--> 350

1 5 10 15 Phe Thr Asp Asp Ala Ile Gln Glr

352 <210> SEQ ID NO: 18
353 <211> LENGTH: 36
354 <212> TYPE: PRT
355 <213> ORGANISM: Caenorhabditis elegans
357 <220> FEATURE:
358 <223> OTHER INFORMATION: Flag Epitope
360 <400> SEQUENCE: 18
361 Val Ile Asp Thr Lys Trp His Tyr Leu Gly Pro Asp Ser Glu Lys Tyr

Same

E--> 362

1 5 10 15 Gly Pro Tyr Met Ser Lys Asp Met

364 <210> SEQ ID NO: 19
365 <211> LENGTH: 35
366 <212> TYPE: PRT
367 <213> ORGANISM: Caenorhabditis elegans
369 <220> FEATURE:
370 <223> OTHER INFORMATION: Flag Epitope

RAW SEQUENCE LISTING
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Input Set : A:\1062.1021-004.TXT
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372 <400> SEQUENCE: 19
373 Val Glu Ser Ser Trp Arg Tyr Ile Asp Thr Gln Gly Gln Ile His Gly

E--> 374

1 5 10 15 Pro Phe Thr Ile Gln Met Met Ser
376 <210> SEQ ID NO: 20
377 <211> LENGTH: 35
378 <212> TYPE: PRT
379 <213> ORGANISM: Saccharomyces cerevisiae
381 <220> FEATURE:
382 <223> OTHER INFORMATION: Flag Epitope
384 <400> SEQUENCE: 20
385 Ile Glu Ser Gln Trp Lys Tyr Ile Asp Ser Asn Gly Asn Ile Gln Gly

Same

E--> 386

1 5 10 15 Pro Phe Gly Thr Asn Asn Met Ser
388 <210> SEQ ID NO: 21
389 <211> LENGTH: 31
390 <212> TYPE: PRT
391 <213> ORGANISM: Saccharomyces pombe
393 <220> FEATURE:
394 <223> OTHER INFORMATION: Flag Epitope
396 <400> SEQUENCE: 21

E--> 397

Trp Leu Tyr Lys Asp Pro Gln Asn Asn Val Gln Gly Pro Phe Thr Gly 1 5
399 <210> SEQ ID NO: 22
400 <211> LENGTH: 21
401 <212> TYPE: PRT
402 <213> ORGANISM: Homo sapiens
404 <220> FEATURE:
405 <223> OTHER INFORMATION: Flag Epitope
407 <400> SEQUENCE: 22

Same

E--> 408

Pro Pro Pro Pro Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro 1 5
410 <210> SEQ ID NO: 23
411 <211> LENGTH: 62
412 <212> TYPE: PRT
413 <213> ORGANISM: Homo sapiens
415 <220> FEATURE:
416 <223> OTHER INFORMATION: Flag Epitope
418 <400> SEQUENCE: 23
419 Asp Val Met Trp Glu Tyr Lys Trp Glu Asn Thr Gly Asp Ala Glu Leu
420 1 5 10 15
421 Tyr Gly Pro Phe Thr Ser Ala Gln Met Gln Thr Trp Val Ser Glu Gly
422 20 25 30

Same

E--> 423

Tyr Phe Pro Asp Gly Val Tyr Cys Arg Lys Leu Asp Pro Pro Gly Gly 35 40
425 <210> SEQ ID NO: 24
426 <211> LENGTH: 31
427 <212> TYPE: PRT
428 <213> ORGANISM: Homo sapiens
430 <220> FEATURE:
431 <223> OTHER INFORMATION: Flag Epitope
433 <400> SEQUENCE: 24

E--> 434

Trp Tyr Tyr Lys Asp Pro Gln Gly Glu Ile Gln Gly Pro Phe Asn Asn 1
436 <210> SEQ ID NO: 25

5

RAW SEQUENCE LISTING
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DATE: 06/20/2001
TIME: 12:29:35

Input Set : A:\1062.1021-004.TXT
Output Set: N:\CRF3\06202001\I873106.raw

437 <211> LENGTH: 31
438 <212> TYPE: PRT
439 <213> ORGANISM: HOMO sapiens
441 <220> FEATURE:
442 <223> OTHER INFORMATION: Flag Epitope
444 <400> SEQUENCE: 25

Sam²

E--> 445

Gln Trp Phe Ser Arg Ser Leu Ala Pro Cys Pro Gly Pro Phe Thr Thr 1

5

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/873,106

DATE: 06/20/2001
TIME: 12:29:36

Input Set : A:\1062.1021-004.TXT
Output Set: N:\CRF3\06202001\I873106.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:177 M:252 E: No. of Seq. differs, <211>LENGTH:Input:341 Found:320 SEQ:2
L:185 M:252 E: No. of Seq. differs, <211>LENGTH:Input:26 Found:0 SEQ:3
L:193 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:4
L:201 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:5
L:209 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:6
L:217 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:225 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:0 SEQ:8
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:257 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:269 M:252 E: No. of Seq. differs, <211>LENGTH:Input:6 Found:0 SEQ:10
L:282 M:252 E: No. of Seq. differs, <211>LENGTH:Input:70 Found:48 SEQ:11
L:315 M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:0 SEQ:14
L:326 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:338 M:252 E: No. of Seq. differs, <211>LENGTH:Input:38 Found:16 SEQ:16
L:350 M:252 E: No. of Seq. differs, <211>LENGTH:Input:34 Found:16 SEQ:17
L:362 M:252 E: No. of Seq. differs, <211>LENGTH:Input:36 Found:16 SEQ:18
L:374 M:252 E: No. of Seq. differs, <211>LENGTH:Input:35 Found:16 SEQ:19
L:386 M:252 E: No. of Seq. differs, <211>LENGTH:Input:35 Found:16 SEQ:20
L:397 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:408 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:22
L:423 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:32 SEQ:23
L:434 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:445 M:333 E: Wrong sequence grouping, Amino acids not in groups!